#### Kemmerer, Elizabeth

From:

Kemmerer, Elizabeth

Sent:

Thursday, June 19, 2003 2:29 PM

To: Subject:

Kunz, Gary SPDI favor

Importance:

High

### Hi Gary-

I am currently working on 09/941992, a SPDI case which is a date case. The 2 companion cases are not yet docketed: 09/990711 and 09/991150. They're both in central files on the 12th floor. Can these be docketed to me as well, since it would be easy to write up the 3 cases together, and they're all date cases?

Thanks a bunch,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10D19

### STIC-Biotech/ChemLib

From: Sent:

Kemmerer, Elizabeth Thursday, June 19, 2003 2:30 PM STIC-Biotech/ChemLib

To: Subject:

sequence search request

Please search SEQ ID NO: 20 for 09/941992; regular and interference, please.

Thanks,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10D19

Mary Jane Ruhl
Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:44:16; Search time 38 Seconds

(without alignments)
1606.021 Million cell updates/sec

Perfect score: 2384
Sequence: 1 MWLRWALSLPPSSCLWAEPG.......DEASSSGCSETDSTELASIL 458
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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A\_Geneseq\_101002:\*

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
NO.	Score	Match	re Match Length DB	DB	ID	Description
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m	2375	9.66	458	21	AAY66635	Membrane-bound oro
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OH	Human transporter Protein sequence o Escherichia coli p Dog P-glycoprotein Dog P-glycoprotein Dog P-glycoprotein Dog (PGP) P-glycop RACMV unique short Dog P-glycoprotein Dog P-glycoprotein Dog P-glycoprotein	Lactococcus lactis Human prostate spe Novel bone marrow Human multidrug re Human transmembran Novel human diagno Human BAG-4 protei Lactococcus lactis Human orghan G pro Human G protein co	H. Pylori transpor Cynomologous monke A suppressor of de Novel human diagno Novel human diagno H. Pylori GHPO 699 Helicobacter polyp
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pharmaceutical; receptor immunoadhesin; gene
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This represents a human secreted protein. The specification provides secreted protein sequences (AAM63681 to AAW6369) encoded by the nucleic acid sequences shown in AAV43601 to AAV43699. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular differentiation activity, reemorated growth or regeneration, activin or inhibin activity, chemotactic or chemokinetic activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which express the proteins, or a stage- or disease-specific alteration in protein expression. They proteins. Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that bind specifically to the protein can also be used to be identified using therefore the protein can also be used to be identified using the proteins in screening assays. The proteins and antibodies that bind specifically to the protein can also be used to be also asset which are also be used to be also asset to be also asset which are also be used to be also asset to be also asset which are also asset which are also be used to be also asset which are also be used to be also asset which are also asset when a second and antibodies which are also asset and a second and antibodies which are also asset to a sea
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Pred. No. 2.4e-163;
5; Mismatches 5; Indels 12;
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Matches 362; Conservative
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AAY AAY73325-Y73389 are human transcriptional regulator molecule (HTRM)

protein sequences. The HTRM protein and nucleotide sequences are useful

Co preventing or treating disorders associated with decreased expression

or activity of HTRM which include cell proliferative disorders such as

cateriosclerosis and cirrhosis; cancers including adenocarcinoma and

cateriosclerosis and cirrhosis; cancers including adenocarcinoma and

co arteriosclerosis and cirrhosis; cancers including adenocarcinoma and

co arteriosclerosis, and myasthenia gravis; infections and trauma. Antagonists

co fithe HTRM polypeptides are useful for treating or preventing disorders

co fithe HTRM polypeptides are useful for treating or preventing disorders

co fithe HTRM polypeptides are useful for becenting disorders

co polypeptides, their immunogenic fragments or oligopeptides are useful

co for screening libraries of compounds in drug screening techniques.

Cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating gene function by modulating the activity of

cof mRNA and regulating detect the expression of HTRM.

Cof diagnosing disorders associated with the expression of HTRM.

Cof diagnosing the naturally occurring genemic and to detect

cof individuals. Using diagnostic assays, cancer can be detected prior to

consider the appearance of clinical sassays, cancer can be detected prior to

consider by accreening the activity of the appearance of clinical sassays 
                                                                                                                                                                                                                                                                                                                                             HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosolerosis; oirrhosis; cancer; leuklaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides useful for diagnosis, prevention and treatment of cancer and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O, Lal P, Yue H, Reddy R,
Patterson C, Baughn MR, Azimzal Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 129-130; 193pp; English
435 QALRDEASSSGCSETDSTELASIL 458
                          HTRM clone 156986 protein sequence.
                                                                                                                                                             AAY73370 standard; Protein; 530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0095827.
98US-0102745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US09935
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                                                                                                                                                                                                                                                    24-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-052941/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ52455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09957144-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1999;
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02-OCT-1998;
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Gerstin EH,
                                                                                                                                                                                                           AAY73370;
                                                                                                               RESULT 5
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be prevented by aggressive treatment or preventive measures.

530 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 QADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVRE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEFONLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 TLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKKAL 434
                                                                                                                                                       The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hammonlytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                               disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 530;
                                                                                                                                 Claim 11; SEQ ID NO 2710; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1816; DB 23;
Pred. No. 3.8e-163;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QALRDEASSSGCSETDSTELASIL 458
                                                                                                                                                                                                                                                                                                                                                                                                                   tch 76.2%;
al Similarity 94.3%;
362; Conservative
           Rosen CA;
                                  WPI; 2002-122018/16.
                                                                                                                                                                                                                                                                                                                                                                                             530 AA;
                                               N-PSDB; ABL90743
           Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local
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AAB94114 standard; Protein; 365 AA.

RESULT 8 AAB94114 AAB94114;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide omprises at least 15 nucleotides and the combination of the 5'-end sequence, 3'-end sequence, 3'-end sequence, 10'-end 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 QADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 TCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVG
                                                                                                                                                    detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 990; DB 22;
Pred. No. 3.8e-85;
; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 14354; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagai K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi K,
A, Nagai K
                                                                               Human protein sequence SEQ ID NO:14354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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90.0%;
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
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26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full-length cDNAs
                                                                                                                                                        primer;
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                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                        Human;
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human secreted proteins given in AAF33213 to AAF33261 encode the human secreted proteins given in AAB64882 to AAB64930. AAB64931 to AAB6491 represent human secreted polypeptide sequences and proteins howelves to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antimicroblal; anti-anglogenic; ophthalmological; cardiant; vascular; antimicroblal; anti-anglogenic; ophthalmological; neuroprotectant; anticonvulsant; nootropic; antialzheimers; antiparkinsonian; and vulnerary. The polynucleotides and polypeptide expression. Disorders that may be be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. Disorders that may be prevented, diagnosed and/or treated by the above methods include immune disorders (e.g. multiple solerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. scimitar syndrome, Capada's cardiomyopathy and coronary antiparking and capada's cardiomyopathy and coronary and capada and capada's cardiomyopathy and coronary and capada and capa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 MLVTMAPIVLILLGLLFKMYPIDEERRRQNKKALQALRDEASSSGCSETDSTELASIL 458
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neovascularisation and diabetic retinopathy), neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein sequence encoded by gene 9 SEQ ID NO:125.
                                                        Huntington's chorea, Alzheimer's disease, Parkinson's disease infectious disease; chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 60;
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100.0%; Pred. No. 2.5e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM, Komatsoulis GA;
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     corneal graft neovascularisation;
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Best Local Similarity 100.
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSE/) ROSEN C A.
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                                                                                                                                                                                                                                                                                                                      WO200076530-A1.
                                                                                                                                                                                                                            Homo sapiens.
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The polynucleotide sequences given in AAF3313 to AAF33261 encode the human secreted proteins given in AAB64882 to AAB64930. AAB64931 to AAB64931 represent human secreted polypeptide sequences and proteins condeciles the genes are expressed in the exemplification of the proteins and cells the genes are expressed in the exemplification of the present invention. Human secreted proteins have activities based on the tissues can decilis the genes are expressed in the examples of activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; cardiant; antinflammatory; anticonvulsant; nootropic; antialzheimers; antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can expression in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. Disorders that may be prevented, diagnosed and/or treated by the above methods include immune content of inspections; systemic lupus erythematosus and disorders (e.g. multiple sclerosis, systemic lupus erythematosus and calsorders (e.g. multiple sclerosis, systemic lupus erythematosus and disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases cancers and Gaucher's disease, cardiovascular diseases (e.g. cancers and Gaucher's disease, cardiovascularisation and diabetic retinopathy, neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's diseases), infectious diseases and/or for promoting wound healing, regeneration and coronary coronary coronary sequences and/or for promoting wound healing, regeneration and coronary coronary sequences and/or for promoting wound healing, regeneration and coronary coronary sequences and/or for promoting wound healing, regeneration and coronary 
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                        Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;
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66.2%; Pred. No. 2.7e-10;
iive 5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis
                                                                                                                                                                                                                                                                                                     infectious disease; chemotaxis.
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10-DEC-2001 (first entry)
  Olsen HS,
                        WPI; 2000-106100/09.
                                                                                                                                                                                                                                                                                                                                  secreted proteins.
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                                  N-PSDB; AAZ97034
   Lafleur DW,
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AAE10448
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                                                         13;
                                                                                                                                                                                      205 RENVVRIVAQPSLNIS----LQTLKRNRPLFMLCIGALCVLISTFAVSASSLFYVRYULN 260
                                                                                                                                                                                                                                  DTGLFTVLVLVQNLVGTVASAPLVPGMVARIGKKNTFLIGALLGTCGYLLFFWVSVWSLP 320
                                                                             73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                 253 FRNEFQNLLLAIMLSATL-TIPIWQWFLTRFGKKTAVYVG-ISSAVPFLILVALMESNLI 310
                                                                                                                                                                                                                                                                                                         KFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPID 423
                                                                                                                                                                                                                                                                                                                       | : | : | : | | : || 372 KCGQAIGGSIPAFILGLSGYIANQVQTPE-VIMGIRTSIALVPCGFMLLAFVIIWFYPLT 430
                                                                                                  LGLCYSLVNIPYGSLATAMT00--POSRARLGAARGIAAS--LTFVCLAFLIGPSIK--- 171
                                                                                                                                                 204
                                                                                                                                                                     193 REQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLG 252
                                                                                                                                                                                                                                                              311 ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG-----TEPIFFSFYVFFT 363
                                                                                                                                                                                                                                                                                    VALVALAIASIGOGVTMTVMWALEADTVE-----YGEYLTGVRIEGLTYSLFSFTR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosolerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
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                                                                                                                         133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV
                                                                                                                                                -----NSSPEEMVSVYH-----FWTIVLAIAGMV--LYFIC----FKST
                                                         Gaps
                                                         63;
                                   Length 457;
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Mucenski M,
                                 Score 143.5; DB 19; Length: Pred. No. 7.5e-05; 62; Mismatches 178; Indels
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Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein HKFBC53, SEQ ID NO:145
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Brewer LA, Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY86230 standard; Protein; 443 AA.
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98US-0089508.
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98US-0089510.
98US-0090112.
                                 6.0%;
19.8%;
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                                                         Conservative
                                            Similarity
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          457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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22-JUN-1998;
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Best Local (
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AAY86115 to AAX86333 are the secreted proteins encoded by the 94 human genes. AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human genes. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Also pathological conditions and be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 94 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and fictancies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atheroscierosis, diabetes, cardiovascular disorders, kidney disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AQGLAPGRHRLRPAVLPLHLQPLPGLWGGHAEWAALLYYGPFIVIFQFGWASTQISHLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGVREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 REPYEAQOSEPIAYFRGLRLVMSHGPYIKLITG------FLFTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 RRPHAEEPGE-------HTPLLAPATAQPLLWKHWLREPAFYQVGILYMTTRL
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                                                                                                                                                                    New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Komatsoulis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 132; DB 21;
; Pred. No. 0.00089;
46; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SSGSCPTSHTARPIGTCFSIASL-----KQWSRVSMF-
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Moore PA,
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 400-402; 586pp; English.
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Shi Y,
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Best Local Similarity 19.8%
Matches 77; Conservative
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us-09-941-992-20.rai

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(without alignments)
518.296 Million cell updates/sec
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1 WWLRWALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL 458
                                                                                                                           June 19, 2003, 17:46:17; Search time 26 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                             262574 seqs, 29422922 residues
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/pcryuS\_COMB.pep:/
/cgn2\_6/ptodata/1/iaa/backfiles1.pep:\* Issued\_Patents\_AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		dР			COLUMNIC		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
	143.5	6.0	457	1 8	US-08-882-704A-6	Sequence 6, Appli	
7	143.5	9.0	457	7	US-09-151-957-6	Sequence 6, Appli	
m	128.5	5.4	456	9	5432081-7	Patent No. 5432081	
4	120.5	5.1	4	9	5432081-9	Patent No. 5432081	
Ŋ	109	4.6	457	m	US-09-416-213-2	7	
9	109	4.6	4	7	US-09-416-214-2	7	
7	109	4.6	457	4	US-09-035-676-2	Sequence 2, Appli	
œ	107.5	4.5	1280	7	US-08-752-447-2	7	
σ	107.5	4.5	1280	4	US-09-316-167-2	• •	
10	107	4.5	426	9	5268463-8		
11	106.5	4.5	1280	7	US-08-583-276-19	Sequence 19, Appl	
12	106.5	4.5	1280	9	5206352-4	Patent No. 5206352	
13	106	4.4	580	7	US-08-677-049-12	Sequence 12, Appl	
14	103	4.3	457	9	5268463-7	Patent No. 5268463	
15	101	4.2	460	Н	. US-08-689-974-5	Seguence 5, Appli	
16	101	4.2	460	m	US-09-058-376-5	'n	
17	97.5	4.1	822	4	US-08-684-932A-38	Sequence 38, Appl	
18	96.5	4.0	364	S	PCT-US96-10618-2	7	
19	96	4.0	1279	7	US-08-784-649A-2	2	
20	95.5	4.0	445	4	US-09-134-001C-3507		
. 21	95	4.0	435	9	5268463-9		
22	95	4.0	436	9	5432081-10	Patent No. 5432081	
23	94.5	4.0	290	4	US-09-134-001C-4893	Sequence 4893, Ap	
24	93.5	3.9	369	4	US-09-172-353-6	Sequence 6, Appli	
52	93.5	3.9	384	4	US-09-200-673-15		
56	93	3.9	808	4	US-09-134-001C-3105		
27	92.5	3.9	383	m	US-09-045-186-2		

13;

133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV 192

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sequence 4, Appli Sequence 15, Appl Sequence 3, Appli Sequence 2, Appli Sequence 16, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 7, Appli
US-08-232-144-4 US-08-55-268A-15 PCT-US33-05039-3 US-08-846-766-5 US-08-76-55-6 US-08-76-576-10 US-09-134-001C-5576 US-09-556-706B-2 US-09-328-59A-1 PCT-US95-04611A-19 US-09-513-057C-3 US-09-513-057C-3 US-09-513-057C-3 US-09-513-057C-3 US-09-513-057C-3 US-08-998-976-4 US-08-898-976-4 US-08-898-976-4 US-08-898-976-4
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## ALIGNMENTS

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73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRWTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 457;
                                           GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Leader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                     SPETWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/882,704A
                                                                                                                                                                                              ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 143.5; DB 2;
19.8%; Pred. No. 2.1e-05;
ttive 62; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-JUN-1997
CLASSIFTCATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: NO. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application US/08882704A Patent No. 5879906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 457 amino acids TYPE: amino acid
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Best Local Similarity 19.8%
Matches 75; Conservative
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linear
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US-08-882-704A-6
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CLASSIFICATION:
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                                                                                             94010
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                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRWTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 LGLCYSLVNIPYGSLATAMTQQ--PQSRARLGAARGIAAS--LIFVCLAFLIGPSIK--- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 LMESNLIITYAVAVAAGISVAAAFILPWSMLPDVIDDFHLKQPHFHG------TEPIFF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLL 416
SFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLL 416
                                   364 SLFSFTRKCGQAIGGSIPAFILGLSGYIANQVQTPE-VIMGIRTSIALVPCGFMLLAFVI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 FRNEFQNLLLAIMLSATLTIPIW------QWFLTRFGKKTAVYVG-ISSAVPFLILVA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 DTGLFTVLVL------VQNPGWYCGIGTAGAXMVARIGKKNTFLIGALLGTCGYLLFFW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 SLESFTRKCGQAIGGSIPAFILGLSGYIANQVQTPE-VIMGIRTSIALVPCGFMLLAFVI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 VSVWSLPVALVALAIASIGQGVTMTVMWALEADTVE------YGEYLTGVRIEGLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 428;
                                                                                                                                                                                                                            APPLICANT: JEFFERSON, RICHARD A.
TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLISCUCORONIDE PERMEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 120.5; DB 6; Length
; Pred. No. 0.003;
58; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suppressors of Death Domains
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,546
FILING DATE: 15-0CT-1993
PRIOR APPLICATION NUMBER: 447,976
FILING DATE: 31-0CT-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-0CT-1988
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
                                                                         417 FKMYPIDEERRRQ-----NKKALQ 435
                                                                                             423 IWFYPLTDKKFKEIVVEIDNRKKVQ 447
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Patent No. 6110690
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goeddel, David V. APPLICANT: Jang, Yingping TITLE OF INVENTION: Suppress NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 IWFYPLTDKKFKE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                            5432081
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357
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                                                                                                                                                                                                              Patent No.
                                                                                                                                                                    RESULT 4
5432081-9
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HTARPIGTCFSIASLKQWSRVSMFPTRLS------PCSSATEQTERDSATAYRMTVE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 PPSPPV-----QPKDSSYPYSQSDQSMNRHNFPCS--VHQYE-SSGTVNNDDSD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 PSSCLWAEP---GMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSGSCPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Jiang, Yingping
TITLE OF INVENTION: Suppressors of Death Domains
TUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.6%; Score 109; DB 3 Best Local Similarity 29.8%; Pred. No. 0.042; Matches 45; Conservative 18; Mismatches
TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VLGTVLGTAIQGQIVGQA--DTPCFQDFNSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLDSQVQYSAEPQLYGNATSDHPNNQDQSSS 364
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/416,213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T98-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/035,676
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09416214
Patent No. 6413728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
3: SCIENCE & TEC
75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 457 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-416-213-2
                                                                                                                                    ZIP: 94010
COMPUTER READABLE FORM:
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                                                  HILLSBOROUGH
                                                                            CALIFORNIA
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OPERATING SYSTEM:
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19;

170

304

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ISPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGOKKELERYNKN 280
                                                                                                                                                                                                                                                                                                                                                                                                              332 LTVFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389
                                              115 MTVEVLGTVL---GTAIQGQIVGQ-----ADTPCFQDFNSSTVASQSANHTHGTTSHRE- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TRGCSQPERVKFT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GNLEFRNVHFSYP----SRKEVKILKGLNLKVQSGQTVALVGNS 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 IGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NSSPEEMVSVYH-----FWTIVLAIAGMV--LYFIC----FKST 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 DIGLETVLVL-----VQNPGWYCGIGTAGAXMVARIGKKTFLIGALLGTCGYLLFFWV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRNEFONLLLAIMLSATLTIPIW------QWFLTRFGKKTAVYVGISSAVPFLILVAL 304
                                                                                                                                                        171 LNTRLTDDVSKINEGIGDKI--GMFFQSMA-----TFFTGFIVGFTRGWKLTLVILA
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                                                                                 51 MVVGTLAAIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMNLEED
                                                                                                                                                                                                                    RGLRLV-----MSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIM
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      67; Mismatches 148; Indels 131; Gaps
                                                                                                                                166 -TQKAYL---LAAGVIVCIYIICAVILILGVRE----QREPYEAQQSEPIAYF---
                                                                                                                                                                                                                                                                                                    LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 INMLVIMAPIVLILIGLLIFK----MYPIDEERRRQNKKALQALRDEASS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JEFFERSON, RICHARD A. TITLE OF INVENTION: PLAANT PROMOTER A-GLUCURONIDASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%; Score 107; DB 6; I
19.0%; Pred. No. 0.059;
Live 59; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 --VFFTKFASGVSLGISTLSLDF----AGYQ----
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APPLICATION NUMBER: US/07/447,976
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
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Best Local Similarity 19.08
Matches 71; Conservative
      Conservative
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NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5268463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 426
      Matches . 84;
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5268463-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligcal Agents Specific for P-glycoprotein
                                                                                                                                                                 221 ISPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKELERYNKN 280
                                                                                                                                                                                                                                                          331
                                                                                                                                                                                                                                                                                                                                   332 LIVFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389
MTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGE 170
                                          RGLRLV-----MSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIM 265
                                                                                                                                                                                                                                                                                                                                                                                                                            -----GNLEFRNVHFSYP----SRKEVKILKGLNLKVQSGQTVALVGNS 429
                                                                                                                                                                                                                                                                                                360 --VFFTKFASGVSLGISTLSLDF-----AGYQ-------TRGCSQPERVKFT 397
                                                                                                                                                                                                                                                                                                                                                                                  398 LNMLVTMAPIVLILLGLLLFK----MYPIDEERRRQNKKALQALRDEASS------S 444
                                                                                 171 INTRITDDVSKINEGIGDKI--GMFFQSMA-----TFFTGFIVGFTRGWKLTLVILA
                                                                                                                                                                                                                                          MESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.5; DB 4; Length 1280; Pred. No. 0.27;
                                                                                                                            LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/316,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95,1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6365357nan, Kevin E
RATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09316167
Patent No. 6365357
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mechetner, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | :: : |
430 GCGKSTTVQL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 GCSETDSTEL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREE:
CITY: Chicago
STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90909
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CITY: Ch
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310 FFWVSVWSLPVALVALAIASIGOGVTMTVMWALEADTVE-----YGEYLTGVRIEG 360
                                                                                                                                                                                                                                                                                SATLTIPIW-QWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 VGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILLIGV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 REQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRNEFQNLLLAIMLSATLTI---PIW-----QWFLTRFGKKTAVYVG-ISSAVPFLI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 IFFSFYVFFTKFASGVSLGISTLS---LDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 IMMESIGDITATCDVSRLQVEGATFDSRIQGGVLGNGITCLLAGLCTITPMSVFAQNNGV 411
                                                                                                                    148 TVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPI 207
                                                                                                                                                                                                 AYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEF-QNLLLAIML 266
                                                                                                                                                                                                                                      AKF-AAALVAIPSSVLGGMTTFLFSSVAISGVR----IMCSVDWTRRNRFILTASFAVGM 491
                                                                                                                                                                                                                                                                                                                     492 AATL-VPDWFSYFFTYSGDNHAL-EGLLQAV------ELVMANGFAVTGFLGLLL 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 IGTCFSIASLKQWSRVSMFPTŘLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LNDTGLPTVLVLVQVPGWYCGIGTAGAXMVARIGKKNTFLIGALLGTCGYLL 309
292 MKSCAVIVGLLVGCIVAAACGYFDRSGIDAAPVASFIWVKTFPLTIYAPLILPLLAVYMV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG-----TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------NSSPEEMVSVYHFW------TIVLAIAGMVLYYFIC----FKST
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                                                                                                                                                            ---YCCCFFLVVMGI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JEFFERSON, RICHARD A.
TITLE OF INVENTION: PLAANT PROMOTER A-GLUCURONIDASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168;
                                       100 SATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVGQADT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 103;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/447,976
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                               326 AFLLPWSMLPDVID 339
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Best Local Similarity 18.99
Matches 74; Conservative
                                                                                                                                                         412 IALTPCANRKAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No. 5268463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;SEQ ID NO:7:
; LENGTH: 457
5268463-7
                                                                                                                                                                                                 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches 133; Indels 120;
                                                                                                                                                                                                           APPLICANT: Guimares, M. Jorge
APPLICANT: Bazan, J. Fernando
APPLICANT: McClanahan, Terrill K.
APPLICANT: Zlotnik Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---VSMFP-TRLSP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region
LOCATION: 437..499
OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10
OTHER INFORMATION: of Figure 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 WASAS---ANPPGPAWVALCPGSSSPRPWPSLPTSSS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encompasses TM 4 of Figure 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIS TYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 106; 21.4%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TSHTARPIGT --- CFSIASLKQWSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,049
FILING DATE: 03-UL-1996
CLASSIFICATION: 435
                                                                                                                                                       Sequence 12, Application US/08677049 Patent No. 5858707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 580 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 21.49
nes 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                       :: : : 1
432 GKSTTVQL 439
                447 SETDSTEL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                       US-08-677-049-12
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Matches
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

June 19, 2003, 17:48:07; Search time 25 Seconds

(without alignments)

1982.349 Million cell updates/sec

Perfect score:
2384
Sequence:
1 MWLRMALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL 458
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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4: /cgn2\_6/ptodata/1/pubpaa/USOG\_NEW\_PUB.pep:\*
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6: /cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*
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14: /cgn2\_6/ptodata/1/pubpaa/USOB\_PUBCOMB.pep:\*

Published\_Applications\_AA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	æ					
Score	Query Match	Length DB	DB	ID	Description	
384	100.0	458	. 6	US-09-992-598-20	Seguence 20.	Appl
384	100.0	458	σ	US-09-989-293A-20	Sequence 20.	Appl
2384	100.0	458	6	US-09-989-735-20	Sequence 20.	Appl
2384	100.0	458	σ	US-09-990-444-20	Sequence 20,	Appl
2384	100.0	458	σ	US-09-989-730-20	Sequence 20,	Appl
2384	100.0	458	σ	US-09-990-436-20	Sequence 20,	Appl
2384	100.0	458	σ	US-09-991-181-20	Sequence 20,	Appl
2384	100.0	458	6	US-09-993-687-20	•	Appl
2384	100.0	458	δ	US-09-989-734-20		Appl
2384	100.0	458	δ	US-09-997-653-20	Sequence 20,	Appl
2384	100.0	458	σ	US-09-993-667-20		Appl
2384	100.0	458	σ	US-09-990-438-20		Appl
2384	100.0	458	6	US-09-990-562-20		Appl
2384	100.0	458	6	US-09-997-428-20		Appl
2384	100.0	458	6	US-09-997-666-20	Sequence 20,	Appl
2384	100.0	458	6	US-09-990-711-20	Sequence 20,	Appl
2384	100.0	458	6	US-09-989-726-20		Appl
2384	100.0	458	σ	US-09-990-437-20	Sequence 20,	Appl
2384	100.0	458	σ	US-09-998-156-20	Sequence 20,	Appl

20         2384         100.0         458         9         US-09-991-157-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-514-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-514-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-514-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-514-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-512-0         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-559-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-559-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-997-559-20         Sequence 20, Sequence 20, 239         2384 100.0         458         9         US-09-991-854-20         Sequence 20, Sequence 20, 2384 100.0         458         9         US-09-991-442.0         Sequence 20, 20, 234-20         Sequence 20
2384         100.0         458         9         US-09-991-157-20           2384         100.0         458         9         US-09-991-172-20           2384         100.0         458         9         US-09-997-514-20           2384         100.0         458         9         US-09-997-514-20           2384         100.0         458         9         US-09-997-514-20           2384         100.0         458         9         US-09-997-5126-20           2384         100.0         458         9         US-09-997-612-20           2384         100.0         458         9         US-09-997-624-20           2384         100.0         458         9         US-09-991-84-20           2384         100.0         458         9         US-09-991-84-20           2384         100.0         458         9         US-09-991-440-20           2384         100.0         458         9         US-09-997-628-20           2384         100.0         458         9         US-09-997-628-20           2384         100.0         458         9         US-09-997-628-20           2384         100.0         458         9         US-09-9
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# ALIGNMENTS

RESULT 1 115-09-992-598-20	Sequence 20, Application US/09992598 Patent No. US2002016038481	GENERAL INFORMATION:	APPLICANT: Ashkenazi, Avi J.							: Gerber, Hanspere		Goddard, Audrey	APPLICANT: GOGOWSKI, Faul J. ADDITOANT: Grimald: Thristopher		: Kliavin, Ivar		APPLICANT: Pan, James	APPLICANT: Paoni, Nicholas F.				: Watanabe,		: Wood, Will	ANT: Zhang, Zemin	INVENTION: Secreted and Transme	TITLE OF INVENTION: Acids Encoding the Same	FILE REFERENCE: P2730P1C20	APPLICATION N	z	APPLICATION N		APPLICATION N	FILING DATE: 1997-10	APPLICATION N	FILING DATE: 199/-1.	APPLICATION N	PRIOR FILING DATE: 199/-11-13
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/989,293A CURRENT FILING DATE: 2001-11-20 PRIOR FILING DATE: 1997-06-16 PRIOR FILING DATE: 1997-06-16 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-13 PRIOR FILING DATE: 1997-11-24 PRIOR FILING DATE: 1998-02-25 PRIOR FILING DATE: 1998-03-20 
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R APPLICATION NUMBER: 60/088039
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/087607
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-04-28
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-04
                                                                                               Watanabe, Colin K.
Williams, P. Mickey
                                                   Timothy A
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                                                                                                                                                Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                        rumas, Daniel
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ive 0; Mismatches 0;
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R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091978
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R FILING DATE: 1998-07-07
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                                              APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
                                                                                               APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/091544
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Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker, Kevin P.
Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 458; Conservative
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APPLICANT: Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-293A-20
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R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
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R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
                                                  FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
PLICATION NUMBER: 60/088033
LING DATE: 1998-06-04
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LING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089105
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PLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
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PLICATION NUMBER: 60/089598
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FILLING DAFE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILLING DATE: 1998-06-23
                                     PLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/989,735
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R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
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R PILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/049787
FILING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
               Application US/09989735 to. US20020193299A1
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FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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NG DATE: 1998-02-25
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FILING DATE: 1998-04-28
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088029
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Ferrara, Napoleone
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                                             GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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PRIOR PRILING DATE: 1998-06-24
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A APPLICATION NUMBER: 60/090252

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R FILING DATE: 1998-06-22

A APPLICATION NUMBER: 60/090349

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R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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360 61 SGSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATATRWTVEVL 120 241 GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300 9 9 SGSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVL LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYV 1 MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSS YIICAVILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVE 241 GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI FFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMY Gaps .; 0 Length 458; PIDEERRRONKKALQALRDEASSSGCSETDSTELASIL 458 100.0%; Score 2384; DB 9; 100.0%; Pred. No. 5.4e-185; ive 0; Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/090862
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091519
PRIOR PAPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07 Sequence 20, Application US/09990436 Publication No. US20020198148A1 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09 Baker, Kevin P. Botstein, David Desnoyers, Luc Eaton, Dan L. Query Match 100. Best Local Similarity 100. Matches 458; Conservative APPLICANT: Ashkenazi, Avi J. RESULT 6 US-09-990-436-20 APPLICANT: APPLICANT: APPLICANT: APPLICANT: 301 301 361 361 421 421 δ g 셤 ò g ò

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                                                                             FFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMY
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PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-34
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084500
PRIOR FILING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-02
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Gurney,Austin L.
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Watanabe, Colin K.
Williams, P. Mickey.
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A
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Fong, Sherman
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Goddard, Audrey
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Botstein, David
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                                                                     PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR APPLICATION NUMBER: 60/090540
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/090863
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PRIOR APPLICATION NUMBER: 60/091978
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PGC11 CURRENT APPLICATION NUMBER: US/09/993,687
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PRIOR APPLICATION WUMBER: 60/065186
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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PRIOR APPLICATION NUMBER: 60/08332
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
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IOR FILING DATE: 1997-11-24
IOR APPLICATION NUMBER: 60/075945
IOR FILING DATE: 1998-02-25
IOR APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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RIOR APPLICATION NUMBER: 60/088033
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IOR APPLICATION NUMBER: 60/065311
IOR FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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                                                                         Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Roy, Margaret Ann
Stewart, Timothy A
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/088734
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Length 458; Indels 100.0%; Score 2384; DB 9; 100.0%; Pred. No. 5.4e-185; Mismatches APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 LING DATE: 1998-06-24 PLICATION NUMBER: 60/090540 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILLING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/090444 60/090445 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090542 LICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090694 ; 0 PLICATION NUMBER: 60/ LING DATE: 1998-06-23 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-25 1998-06-25 1998-06-24 998-06-24 998-07-02 1998-07-07 LING DATE: 1998-07-01 998-07-02 2-90-866 LING DATE: 1998-06-3 1998-06-Query Match 100. Best Local Similarity 100. Matches 458; Conservative FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: LING DATE: LING DATE: LING DATE: LING DATE:

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R APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090863
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FILING DATE: 1998-07-02
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FILING DATE: 1998-06-24
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                  Gaps
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                                                                                      Length 458;
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0; Mismatches 0;
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                     100.0%;
100.0%;
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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                                                                                   Query Match
Best Local Similarity 100.0
Matches 458; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/065186
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Williams, P. Mickey
Wood, William I.
                Perrara, Napoleone
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Stewart, Timothy
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Gerritsen, Mary E.
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                                                                             Goddard, Audrey
Godowski, Paul
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Live 0; Mismatches 0;
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APPLICATION NUMBER: 60/092182
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           FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/090863
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
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Best Local Similarity 100.
Matches 458; Conservative
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Database :

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SUMMARIES	ΩI		GUTA_BACSU	XYLP_LACPE	UIDB_ECOLI	YJMB_BACSU	RAFP_PEDPE	YNAJ_BACSU	SHIA_ECOLI	YAGG_ECOLI	LACP_STAXY	YCR3_ERWHE	YIHO_ECOLI	POLG_MVEV	EXUT_BACSU	BAG4_HUMAN	MDR1_HUMAN	GPT_HUMAN	UAPC_EMENI	MVIN_BORBU	YIHO_SALTY	YHC8_YEAST	MELB_SALTY	VPP3_HUMAN	RPB1_DROME	CCMF_RHOCA	AMYH_YEAST	CSCB_ECOLI	GPT_CRIGR	GPT_MOUSE	PRO1_LEIEN	CDX4_HUMAN	YXIO_BACSU	WZYE_SALTY
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	Query Match	9.3	6.4	6.1	9	5.8	•		5.5	5.3	5.2	4.7	4.6	4.6	4.6	4.6	4.5	4.4	4.4	4.4	4.4	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1
	Score	221.5	153.5	146	143.5	138.5	138	3		126.5	125	112	110	110	109.5	109	106.5	106	106	105.5	105	101.5	101	101	101	100.5	100.5	100	66	66	an a	98.5	98.5	98.5
	Result No.	П	7	m	4	ι.	9	7	80	on !	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29	30	31	32	33

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NCBI_TaxID=562;
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339 FIWLFASGFFTTPLNTLAWGMVADCVDYAEWKT----GIRADGVVISSMSFINKLGVALA 394
                                             395 GSFSAIXLGIAGY----VANTDOTVASLNAIKNMNALIPGFFILLSIILIAFYPLTERR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (OCT-1998) to the EMBL/GenBank/DDBJ databases:
-!- FUNCTION: RESPONSIBLE FOR TRANSPORT OF XYLOSE INTO THE CELL, WITH
-! THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- SUBGELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                           371 LGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIV---LILLGLLLFKMYPIDEER
                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, sequence analysis, and characterization of the genes involved in isoprimeverose metabolism in Lactobacillus pentosus."; J. Bacteriol. 180:2312-2320(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                             cnaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W., Pouwels P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W., Pouwels P.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 14b; Du., 20.9%; Pred. No. 0.0042; 1ive 68; Mismatches 157; Indels
                                                                                                                                                                                                                                  Lactobacillus pentosus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID-1589;
                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Putative xylose-proton symporter (Xylose transporter).
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                                                                                                                                  479 AA.
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InterPro; IPR003662; sub_transporter.
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TIGRFAMS; TIGR00792; gph;
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Matches 85; Conservative
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479 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                340 DFHLKQPHFHG--TEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVKFT 397
                                                                                                   170 TIRQFMGT-LGATIISTIALPLVAYFGGGSTSS-----AHG------WFMVALIMA
                                                                                                                                                                                                                                                      119 VLGTVLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIV
                                                                                                                                                                                                                                239 VEGNFVLFCTYTLGFRNEFQ-------NLLLAIMLSATLTIPIWQWFLTRF
                                                                                                                                                                                                                                                                                                                283 GKKTAVYVGISSA-VPFLILVALMESNLIITYAVAVAAGISVAAAFL--LPWSMLPDVID
                                                                                                                                                                                                                                                                                                                                                     315 GKRNTMLMGMLLAIVGQLILWGGSKALNVPTITVGTIVGY-LGTGFVSGLIAVMLADSVD
                                                                                                                                                                                       214 VIAMVIFFIVFANTKERVQTVQSKKSIPIK--TSLKALKRNWPWVIVI--FI-----
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STRAIN=KIZ / MG1657;
PubMed=9278503;
Blattiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura T., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jefferson R.A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 LNMLVTMAPIV --- LILLGLLLFKMYPI ---- DEERRRQNKKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UIDB_ECOLI STANDARD; PRT; 457 AA. 130868; P77457; 01-001-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 40, Last annotation update) 01-NOV-1006 (Rel. 40, Last annotation update) 01-NOV-1006 (Rel. 40, Last annotation update) 01-0006 (Rel. 40, Last annotation update) 01-0006 (GUSBOR UIDB OR GUSBOR UIDP OR B1616.
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Jefferson R.A., Burgess S.M., Hirsh D.;
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PRELIMINARY SEQUENCE OF 1-112 FROM N.A.
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Science 277:1453-1474(1997).
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                                                                                                                                                                                                       SSATEQTE-RDSATAYRMTVEVLGTVLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHT 157
                                                                                                                                                                                                                                  158 HGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPIAYFRGLRLVM 217
                                                                                                                                                                                                                                                  193 -------GYPVVMGLFAALGVFWFYICYRNCKERIIISEAPK-EKLTLSSVVKTFI 240
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                                                                                                                                                                                                                                                                                                                                                             218 SHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQW
                                                                                                                                                                                                                                                                                   278 FLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDV
                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pediococcus
                                                                                                                                                                         33;
                                                                                                                                                    h Similarity 18.9%; Score 138.5; DB 1; Length 459; Similarity 18.9%; Pred. No. 0.013; 53; Conservative 70; Mismatches 167; Indels 33;
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                                                                                                                                    B807795C3276E1E3 CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Raffinose carrier protein (Raffinose permease).
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01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                    50420 MW;
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           proteome
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P43466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 YSFKDVGFW---SMLP-----SLTTDSREREKTATFAR------LGSTIGGGLVGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 DTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILI-----L 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 FTIAGSNLWLVLLAATMFGFPQQMVFLVVLMVITDSVEYGQLKLG--HRDESLALSVRPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTKFASGVSLG----ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VMPAVIFFSAKATS-----TGDNR------GWFIFALIICLIALISAWGVGL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYT 250
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                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY HPR) (BY SIMILARITY). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 GTREVDSDIRKNKQDTVGVMEIFKALAKNDQLLWAALAYLFYGVGINILGSLEVYYFTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGFRNEFQ-----NLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 VALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVF
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                                                                                                                                                                                                                                                                                                                               fransmembrane; Sugar transport; Transport; Symport; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 138; DB 1; Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 1.0.,
19.8%; Pred. No. 0.021;
.+ive 61; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15BEC5F69F8C0F61 CRC64;
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 AA
                                                                                                                                                                                                                                                                           PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                EIIA DOMAIN
                                                                                                                                                                                                                                                                                                                                                    SGF DOMAIN
or send an email to license@isb-sib.ch)
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                                                                                                                  InterPro; IPR001927; Na/Gal_symp.
InterPro; IPR001127; PTS_EIIA.
Pfam; PF00389; PTS_EIIA_1; 1.
TIGRPAMS; TGR00792; gph; 1.
TIGRPAMS; TIGR00793; gph; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YMAJ_BACSU STANDARD;
P94488;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
15-JUN-2002 (Rel. 41, Last ann
Hypothetical symporter ynaJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69913 MW;
                                              EMBL; Z32771; CAA83664.1; -. EMBL; L32093; AAA25563.1; -. HSSP; P20166; 1GPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMYPIDEE 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 AA;
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                                                                                                       -----MLANIAHDMVVCVQQPMF--TE-MFGASYRY-----SGAGVGYQVASVVGGGF-- 395
                        272 IPIWQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                                      LLPWSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=KIZ. / MG1657.
STRAIN=KIZ. / MG1657.
PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY (SGF). STRONG, TO E.COLI YICJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Schramm S., Duccan M., Allen E., Araujo R., Aparicio A., Chung E.,
Schramm S., Bederspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U70214; AAB08691.1; ...
EcoGene; EG13346; yagG.
InterPro; IPRO01927; Na/Gal_symp.
TIGRRAMs; TIGR00792; gph; 1.
PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                 386 RGCSQPERVKFTLNMLVTM-----APIVLILLGLLLFKMYPI---DEER 426
                                                                                                                                                                     303 IPCFAWLADREGRRRVYITGTLIGTLSAFPFFMALEAQSIFWIVFFSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                              460 AA
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                                                                                                                                                                                                                                                                         P75683; P71292;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque
16-OCT-2001 (Rel. 40; Last annot:
Hypothetical symporter yagg.
XAGG OR B0270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000135; AAC73373.1; -.
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107
151
180
263
309
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AIQGFAVG-----GEWGGAALLSVESAPKNKKAFYSSGVQVGYGVGLLLSTGLVSLIS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 ---LRHPGAFLKIIALRLCELLTMYIVTAFALNYSTQNMGLPRELFLNIGLLVGGLSCLT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 AIQGQIVGQADTPCFQDFNSSTVAS-QSANHTHGTTSHRETQKAY----LLAAGVIVCIY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ICAVILILG---VR-----EQREPYEAQQSEPIAYFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 RLVMSH-GPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNE-FQNLLLAIMLSATLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Integral membrane protein, Inner membrane.
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakames S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yanamoto Y., Horiuchi T., A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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CYTOPLASMIC (POTENTIAL).
B7FFBBD5AFDAE8CC CRC64;
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CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00083; sugar_tr; 1.
TIGREAMS; TIGR00883; ZA0106; 1.
TIGROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 131.5; DB 22.3%; Pred. No. 0.038; tive 56; Mismatches 1
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PERIPLASMIC (1
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CYTOPLASMIC (
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EcoGene; EG20205; ShiA.
InterPro; IPR004736; Cit_H_symport.
InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                               DNA Res. 3:379-392(1996).
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386
107
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438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 78; Conserv
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TRANSMEM
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                  12;
                                                                                                                                                                                                              167 QKAYLLAAGVIVCIYIICAV-----ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHG 220
                                                                                                                                                                                                                                                                                                                                             279 LTRFGK-----KTAVYVGISSAVPF-----LILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                                                                                                                                                                                                                                                            PPSTLTLTYMLATLPGFIGSYLGAMMYFVTYYLGSASYFMWMLAAHILGKAAGSLLAKRL 111
                                                                                                                                                                                                                                                                                                                                                                                                                LLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRG 387
                                                                                                                                                                                                                                                                              PYIKLITGFLFTSLAFMLVE - GNFVLFCTYTLGFRNEFQNLLLAIMLSATLTIPIWQWF
                                                                                                                                                                                                                                                                                                                                                                            112 TRNFNKVQIFGYCAVLAGVLSIALFFAPKSVFVLVPL-----TFIISTL----YQATT
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                                                                                                                                                                                  Gaps
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 CSQPERVKFTLNMLVTMAPIVLILLGLLLF---KMYPIDEERRRQ-NKKALQAL
                                                                                                                                                                                 64;
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STRAIN=K12 / MG1655;
MEDLINE=93347969; PubMed=8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
**Analysis of the Escherichia coli genome. III. DNA sequence region from 87.2 to 89.2 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                              Score 112; DB 1; Length 27
Pred. No. 0.5;
1; Mismatches 122; Indels
                                                            InterPro; IPR001927; Na/Gal_symp,
PROSITE; PS00872; Na_GALACTOSIDE_SYMP; FALSE_NEG.
Hypothetical protein.
SEQUENCE 272 Aa; 29955 MW; C7C753B416F14AB6 CRC64;
                                                                                                                                                                                                                                    | :| | | | | | | | | OHRWLCLFGV------
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40, Last annotation update)
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                                                EMBL; M87280; AAA64975.1;
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67; Conserva
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YIHO OR B3876.
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l and this statement is not removed. Usage by and for commercial srequires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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305769;
30180V-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1988 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 LWAVGDILNYFWGSNSFTFVMFSCVAFFGTAFVNSLNWALVPDTVD------YGEWK
     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 VLGTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 AIQVYYTQYVL---NDI-NLLSWMGFFSMGCILIGVLLVPL---TVKCFGKKQVYLAGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 SAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG---
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  is in
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Hypothetical protein; Transport; Transmembrane; Inner membrane;
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     as its content
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EMBL; AE000463; AAC76873.1; ALT_INIT
PIR; S40820; S40820.
ECOGENE; EG11841; Yiho.
InterPro; IPR001927; Na/Gal_Symp.
IIGERAMS; TIGR00792; gph; 1.
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                                                                                                                                                                                                                                                               Runst E., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst E., Ogasawara N., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fulita M., Fulita Y., Funas S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappei S., Hosonos S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Raramata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Murita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogiwara A., Oudega B., Park S.H.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nuback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Barro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sato T., Scanlan E., Schleich S., Scrote B., Rose M., Sadie Y., Scorlian E., Schleich S., Scrote R., Scoffone F.,
Scallan E., Schleich S., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Tarkamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Tarkamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Vanamoto K., Yasumoto K., Tarkahi H., Wendler E., Wedler H., Weller M., Danchin A.,
Ry Phi C., Miller M., Panamoto G., the Gram-positive bacterium Bacillus
R., The Complete Genome sequence of the Gram-positive warmust R.,
R., The Complete Genome sequence of the Gram-positive bacterium Bacillus
                                   MEDLINE-98240225; PubMed-9579062;
Rivolta C., Soldo B., Lazarevic V., Joris B., Mauel C., Karamata D.;
"A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
containing a putative 12.3 kb operon involved in hexuronate catabolism
and a perfectly symmetrical hypothetical catabolite-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
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InterPro; IPR003662; sub_transporter.
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TIGRFAMS; TIGR00893; 2A0114; 1.
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                                                                                                                                                                    Microbiology 144:877-884(1998)
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SubtiList; BG13210; exuT.
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320
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                                                                                                                                                                       71 GAKLTLFVAMVVWSLFSGAVALAFGFVSLLIIRILFGMGEGPLSATINKMVNNWFPPTQR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 ISVAAAFL----LPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGIST 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 LGFIGLAAGGFVSDYVYKKTA-RKGVLFSRKVVLVTCLFSSAVLIGFAGLVATTAGAVTL 322
                                                                                                                                                                                                          108 DSATAYRMIVEVLGTVLGTAIQGQIVGQADIPCFQDFNSSIVASQSANHIHGTISHRETQ 167
                                                                                                                                                                                                                                                                                                   16 -SWKVSFVLIMIIGLIWAVLWFKFVKE--KPQETIKEAP-----AIKAETSPGEKIPLTF
                                                                                                                                          62 GSCPTSHTARPIGTCFSIASLKQWSRVSMFPTRL-----SPCSSATEQ-----TER
                                                                                                                                                                                                                                                                                                                                                   22 YIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEFONLLL---AIMLSATLTIPIWQWF
                                                                                                                                                                                                                                                                                                                                                                                   212 YLKQKT-VLFTAFAFFAY--NYILFF-----FLTWFPSYLVDERGLSVESMSVITVIPWI
                                                                                                                                                                                                                                                                                                                                                                                                                        279 LTRFG-----KKTAVYVGISSAVPFLILVALMESNLIITYA--VAVAAG----
                                                                                                                                                                                                                                                                               168 KAYLLAAGVIVCIYIICAVILILGVREQREPYEAQOSEPIAYFRGLRLVMSHGP-----
                                                                                                       Gaps
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Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
"Prevention of constitutive TNF receptor 1 signaling by silencer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
Science 283:1852-1852(1999).
-!- FUNCTION: INHIBITS THE CHAPERONE ACTIVITY OF HSP70/HSC70 BY
PROMOTING SUBSTRATE RELEASE.
-!- SUBUNIT: BIRDS TO THE ATPASE DOMAIN OF HSP70/HSC CHAPERONES.
                                                                                                       Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAG4_HUMAN STANDARD; PRT; 457 AA.
095429; 095818;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
BAG-family molecular chaperone regulator-4 (Silencer of death
                                                                       Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takayama S., Xie Z., Reed J.C.; "An evolutionarily conserved family of Hsp70/Hsc70 molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            131 ASV----IGVTNSGTPLGGAISGPIVGMI------AVAF---
                                    C2E291AF347F7EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 LSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NTAGIIGPALTGFIVDQTGTFSGAFLLAGGLAVF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 VALSVFELYLTGAIYWAVIQDVVDQNNV-----GSVGGFMHFLA-
                                                                                   21.9%; Pred. No. 1.2;
tive 58; Mismatches 133;
                                                                       DB 1;
                                                                       4.68; Score 109.5;
                    POTENTIAL
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J. Biol. Chem. 274:781-786(1999).
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                                    45313 MW;
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                                                                                                       Conservative
.356 3
381 4
422 AA;
                                                                                       Similarity
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                                                                                                       88;
   TRANSMEM
                    TRANSMEM
                                  SEQUENCE
                                                                     Query Match
Best Local
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 19, 2003, 17:45:42; Search time 19 Seconds (without alignments) 2317.346 Million cell updates/sec

US-09-941-992-20 2384 1 MWLRWALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL 458 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hvpothetical prote	н	sugar, proton symbo	H+-symporter homol	sodium-qalactoside	permease of the Na	glucuronide permea		glucuronide permea	r 1	raffinose carrier	H+-symporter homol	Sodium, galactoside	shikimate transpor	probable transport					sodium-galactoside	xyloside transport	Sugar/Na+(H+) simp	drug	probable transport				probable permease	
SUMMARIES	QI	AB2269	S75696	E97320	н69788	H87465	D96985	C90919	н85767	B64918	D69852	S44253	A69888	AC0122	G64962	Н85822	B90976	B91186	A86033	F64752	D87624	в86813	B97324	C75483	AE0507	F91228	S52977	S55316	E86075	D82302
	DB	7	~			~		~	~	~	~	~	0	~	~	~	~	~	0					~					~	~
	Query Match Length I		544	445	463	514	449	457	457	457	459	641	9	477	438	438	438	466	466	460	463	490	458	1136	457	467	272	317	469	541
đ	Query		9.3	6.5	6.4	6.2	6.1	6.1	6.1	9.0	5.8			5.6	5.5	5.4	5.3	5.3	5.3			٠.	4	4.9	4.7	4.7	4.7	4.7	4.7	4.7
	Score	308.5	221.5	154	153.5	147	145	144.5	44	43	138.5	138	-	132.5	131.5	128.5	127.5	127.5	127.5	126.5	126	119		117.5	113	113	112	112	112	112
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476 0 476

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Control to the total	יואליים בירים לגו	tetracycline resis	probable permease	genome polyprotein	hexuronate transpo	cation efflux syst	tetracycline resis	gastric mucin (clo	cationic amino aci	hypothetical prote	transport system p	hypothetical prote	probable amino aci	hypothetical prote	multidrug resistan	transport system p
4000	******	D/1851	S40820	GNWVMV	A69853	H84126	E64665	147141	E69471	AF2115	AE1354	A89880	A10701	T16084	DVHU1	AF1724
c	۹ (	~	N	Н	Н	ď	7	7	ď	7	7	7	~	~		~
110	# V	386	487	3434	422	1093	386	528	531	387	402	265	447	501	1280	402
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00	2 6	3.1	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 3 AB2269 hypothet C. Specie	RESULT 1 AB2269 hypothetical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120) C.Species: Nostoc sp.	stoc sp. (strain PCC 7120)
A; Note: C; Date:	A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002	nym of Anabaena sp. strain PCC 7120 c-2001 #text_change 30-Jun-2002
 R; Kaneko Nakazal	ko, T.; Nakamura, Y.; Wolk, C.P.; Kuri Ski, N.; Shimpo, S.; Sugimoto, M.; Tak	C.P.C.C.S.J.C.B. Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
A; Title A; Refere A; Access	is. 0, 207 215, 2001. e: Complete Genomic Sequence of the Fi rence number: AB1807; WUID:21595285; P sssion: AB2269	Due nes. 0, 202 113, 2021 Affithe Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A: Reference number: AB1807; WID:21595285; PMID:11759840 A; Accession: AB2269
 A;Status: F A;Molecule A;Residues: A;Cross-ref A;Experimer C;Genetics:	oreliminary type: DNA 1-487 <kcnr> Ferences: GB:BA000019; Ital source: strain PCC</kcnr>	PIDN:BAB75404.1; PID:917132839; GSPDB:GN00179 :7120
 A;Gene:	A;Gene: alr3705	
Query Ma Best Loo Matches	12.9%; cal Similarity 25.5%; 92; Conservative 66	; Score 308.5; DB 2; Length 487; ; Pred. No. 1e-15; 68; Mismatches 148; Indels 53; Gaps 10;
ζŎ	93 TRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVGQADTPCFQDFNSSTVASQ	VLGTA1QGQ1VGQADTPCFQDFNSSTVASQ 152
qa	151 TALTP-ELTQDYDERTSLNSFRFAFSIGGSILSLILSKVVLSL	ILSLILSKVVLSL 192
 Qy	153 SANHTHGTTSHRETOKAYLLAAGVIVCIYI	SANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILIIGVREQREPYEAQQSEPI 207
 qq	193 ISDRQQQYIVLAAAICTVISVISLYMCVFGVRERVLAFEAKRIQVEESDSI	ISLYMCVFGVRERVLAFEAKRIQVEESDSI 242
 Oy	208 AYFRGLRLVMSHGPYIKLITGFLFTSLAFM	208 AYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVBGNFVLFCTYTLGF-RNEFQNLLLAIML 266
qq	243 PFFEQLKIVESNRPFLEVIGIYLFSWLGVQ	PFFFQLKIVFSNRPFLFVIGIYLFSWLGVQITASIIPYFVINCWSLPESDVPTTWIAVQG 302
Qy	267 SATLTIPIWQWFLTRFGKKTAVYVGISSAV	SATLTIPINQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIITYAVAVAAGIS 322
qq	303 TALLMLFVWTALSKKIGKKLVYFLGMSS	:    : :     : :       : :       :
Qy	323 VAAAFLLPWSMLPDVIDDFHLKQPHFHG	VAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDF 380
 qa	360 VSTAYLVPWSMIPDVIELDELQTGQRR	:  :
QY	381 AGYQTRGCSQPERVKFTLNMLVTM	AGYQTRGCSQPERVKFTLMLVTMAPIVLILLGLLLFRMYPIDEERRRQNKKAL 434
Db	416 SGFKEAVAGOTTLPIOPESALFAIRIAVGP	SGFKEAVAGQTTLPIQPESALFAIRIAVGPLPTICLIFGLVLTYFYPITREMHAEILLKL 475
 Qy	435 Q 435	

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A;Status: preliminary
A;Molecule type: DNA
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Best Local Sim:
Matches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Solum-galactoside symporter family protein [imported] - Caulobacter crescentus cipium-galactoside symporter family protein [imported] - Caulobacter crescentus c; Species: Caulobacter crescentus c; Species: Caulobacter crescentus c; Date: 20-Apr-2001 #text_change 20-Apr-2001 c; Accession: H8465 c; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647 A; Accession: H87465 A; Accession: H87465 A; Molecule type: DNA A; Residues: 1-514 cSTO>
A; Canel type: DNA A; Residues: 1-514 cSTO>
C; Genetics: 1-514 cSTO>
C; Genetics: 1-514 cSTO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 MGWFIVILLPITVLLAVMTVKEPAAPPQHGKTGLKQYWRLLMR--PSVQRL---LFADLL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMLVEG----NFVLFCTYTLGF-RNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 MGLAPGIAGTLFLFFERIKGFDKTQAGVLLLVYFLAALAGAPLWPMLAKKLGKHKALVV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GISSAVPFLIL----VALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 ---AAVVYAFVQVGAVFMPAGSSVMGMLLLVLAGLPYSAAPVLVRSMMADIGDEERLES- 399
                                                                                                                                                                                    313 YAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHG·-TEPIFFSFYVFFTKFASGVS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFHGTEPIFFSFYVFFTKFASGVSLGIST-LSLDFAGYQTRGCSQPERVKFTLNMLVTMA 405
                                         --- DQAFGFOMTALIYAAVSIVLNLFSFFTVRERIQ 225
                                                                                                        226 PKKRKKQ---GIKKTLSVLFKNKPLLMLISSFLAFAIGFNIKLSTWVYFTYNVHK-EF 281
                                                                                                                                                             ----QNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGIS-SAVPFLILVALMESNLIIT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 ---GVDKTGLLYAIVTGTVKLGYALAVAVFIALGWMGFDPK-VSTPEGDAALIGM-YAIA 454
TPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREQRE 197
                                                                                                                                                                                                                                                                   : |:| | | | :: | | | 339 FIWLFASGFFTTPLNTLAWGMVADCVDYAEWKT----GIRADGVVISSMSFINKLGVALA 394
                                                                                                                                                                                                                                                                                                                                                   198 PYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYTLGFRNEF
                                                                                                                                                                                                                                                                                                                          LGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIV--:LILLGLLLFKMYPIDEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 SSTVASQSANHTHGTTSHRETQKAY--LLAAGVIVCIYIIC----
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  138
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RESULT D96985

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permease of the Na+, galactoside symporter family [imported] - Clostridium acetobutyl C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: D96985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C90919
R;Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                             Solvent-Producing Bacterium
                                                                                                                                     Zeng, Q.; Gibson,
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                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78671.1; PID:g15023572; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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A;Cross-references: GB:BA000007; PIDN:BAB35746.1; PID:g13361790; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 YLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 LFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIMLS-----ATLTIPIWQWFLTRFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 449;
                                                                                                                            R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve
A;Reference number: A96900; MUID:21359325; PMID:21359325
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larity 19.8%; Pred. No. 0.0023;
Conservative 62; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.1%; Score 145; DB 2; I
Best Local Similarity 23.2%; Pred. No. 0.002;
Matches 63; Conservative 49; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 FTLNMLVTMAP-IVLILLGLLLFKMYPIDEER 426
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C,Superfamily: melibiose carrier protein
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C;Superfamily: melibiose carrier protein
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A; Molecule type:
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               Cyccession: D69852
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carrer, N.M.; Changer, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carrer, N.M.; Changer, S.; Brouillet, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Alaute, S.D.; Emmerson, P.T.; Entian, M.; Fujita, N.; Fuma, S.; Galizzi, A.; Galler J., Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Laudber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Togano, V.; Uchiyama, T.; Winters, P.; Wibat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yasu, K.; Yoshida, K.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: D69852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:299110; GB:AL009126; NID:92633472; PIDN:CAB13088.1; PID:92633585
A;Experimental source: strain.168
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NiAlternate names: raffinose permease; raffinose transport protein
C;Species: Pediococcus pentosaceus
C;Species: Pediococcus pentosaceus
C;Species: Pediococcus pentosaceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: S4425;
R;Leenhouts, K.K.J; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
R;Leenhouts, K.K.J; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
A;Description: The sucrose and raffinose operons of Pediococcus pentosaceus PPEL.0.
A;Reference number: S4425
A;Accession: S44253
A;Molecule type: DNA
A;Residues: 1-641 <LEE>
A;Cross-references: EMBL: 232771; NID: 9493728; PIDN: CAA883664.1; PID: 9475964
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 LVKMFGKKRTAMIGFGISVAADLINFMLPSNVYVFTILASIAFIGISIPNGITWALVSDI 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 IDYGEWKSG--ERKEATTYSLFNFSRKLAQSLSGFLSGIGLGIIGY-VPNAVQTAQALIG 417
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 138.5; DB 2; Length 459; 18.9%; Pred. No. 0.0064; tive 70; Mismatches 167; Indels 33
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Matches 6
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H+Symporter homolog ynaJ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D-Inc. 1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: A69888
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber R;Kunst, F; Deno, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M;
A; Ehrlich, S.D; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Funa, S; Galizzi, A; Gal A;Authors: Foulger, D; Krogh, S.; Kumano, M; Kurita, K; Lapidus, A; Hullo, M Koetter, P; Koningstein, G; Krogh, S.; Kumano, M; Kurita, K; Lapidus, A; Lardino A;Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mau Y, M; Ogawa, K; Ogiwara, A, Oudega, B; Rose, M; Sadaie, Y; Sato, T; Scanl A;Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekiguchi, J; Sekowska, A; Seakenchi, M; Tamakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Tohiya T; Winters, P; Wipat, A; Yamamoto, H; Yasumoto, K; Yata, K; Yoshida A;Authors: Yoshikawa, H; P; Zumstein, E; Yoshikawa, H; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
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C;Superfamily: phosphotransferase system glucose-specific enzyme II, factor III homol C;Keywords: sugar transport; transmembrane protein F;485-639/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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                                                                                                                                                                                                                                                                                                                                                77 FSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVGQA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                      YSFKDVGFW---SMLP----SLTTDSREREKTATFAR-----LGSTIGGGLVGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTREVDSDIRKNKQDTVGVMEIFKALAKNDQLLWAALAYLFYGVGINILGSLEVYYFTYI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGFRNEFQ-----NLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI----L 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGKPKSFSILSIINIFLGLI--ATSLFPV----LSKKFSRKGVFAG---CLVFMLGGIAI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 VALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 FTIAGSNLWLVLLAATWFGFPQQMVFLVVLMVITDSVEYGQLKLG--HRDESLALSVRPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 FTKFASGVSLG----ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAVILI-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCTYT
                                                                                                                                                                                                                                                                66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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22.8%; Pred. No. 0.017;
tive 65; Mismatches 138; Indels 82;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A69580; MUID:98044033; PMID:9384377 A; Accession: A69888
                                                                                                                                                                      Query Match 5.8%; Score 138; DB 2; L
Best Local Similarity 19.8%; Pred. No. 0.01;
Matches 73; Conservative 61; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: melibiose carrier protein
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Best Local Similarity 22.8%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KMYPIDEE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 QIFLTEEK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-463 <KUN>
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A;Status: pre-indinary
A;Molecule type: DNA
C;Molecule type: DNA
C;Molec
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K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transport protein, shikimate shiA [imported] - Escherichia coli (strain 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :: |. ::|| | || :| : || 351 --MLANIAHDMVVCVQQPMF--TE-MFGASYRY-----SGAGVGYQVASVVXGGF----- 395
                                                                                                                                                                                 328 LLPWSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQT 385
                                                                                                                                                                                                                                      127 AIQGQIVGQADTPCFQDFNSSTVAS-QSANHTHGTTSHRETQKAY----LLAAGVIVCIY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AIQGFAVG-----GEWGGAALLSVESAPKNKKAFYSSGVQVGYGVGLLLSTGLVSLIS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 I-------ICAVILILGV-----216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 LRHPGAFLKIIALRLCELLTMYIVTAFALNYSTQNMGLPRELFLNIGLLVGGLSCLTIPC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 WQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAFLLP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 WSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGC 388
272 IPIWQWFLTRFGKK----TAVYVGISSAVPFLILVALMESNLIITYAVAVAAGISVAAAF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: H85822
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Escherichia coli
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                   386 RGCSQPERVKFTLNMLVTM-----APIVLILLGLLLFKMYPI---DEER 426
                                                                                                                                                                                                                                                                                                                                                                                                                            89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 438;
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                                                         Query Match

5.4%; Score 128.5; DB 2; Length
Best Local Similarity 21.6%; Pred. No. 0.035;
Matches 75; Conservative 58; Mismatches 125; Indels
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Job time: 22 secs
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H85822
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Run on:

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09cfh0 lactococcus
097dm2 clostridium
09rwc9 deinococcus
08z9n3 salmonella
08x8f0 escherichia
                                                                                                                                         09hed4 neurospora
029070 sus scrofa
0950r4 spitzallomyc
09kub4 vibrio chol
P70939 bacteroides
                                                                                                                                                                                                                                                   O8tmg4 methanosarc
09k6b3 bacillus ha
08s5v1 oryza sativ
025780 helicobacte
                                                                                                                                                                                                                             Q9zk50 helicobacte
Q9q9f7 murray vall
                                                                                                                                                                                                                                                                                                                029071 sus scrofa
028500 archaeoglob
08yu77 anabaena sp
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O46605 canis famil
                                                                                                                                                                                                                                                                                                     Q988c1 rhizoblum 1
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Q8r7f4 thermoanaer
                                                                                                                                                                                                      Q8zrzl salmonella
Q9zb18 lactococcus
                      Q9x425 lactococcus
Q9rav6 lactococcus
                                              Q9rav9 lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 TCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
Wan D.F., Gu J.R.,
"Novel human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN CDNA 1700018018 gene (Hypothetical 58.6 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC011587; AAH11587.1; -. EMBL; AF289609; AAL55793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 530 AA; 58623 MW; 3B6978F4EA92C763 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.2%; Score 1816; DB 4; 94.3%; Pred. No. 1.2e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                        530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
           09A413
09X425
09RAV6
08RAW6
04REM8
046605
09CFH0
097DM2
08Z9W3
08Z9W3
08Z9W3
09Z9W6
09SW6
09SW6
095W8
095W84
                                                                                                                                                                                                                             092K50
0909F7
08TMG4
09K6B3
08S5V1
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                                                                                                                                                                                                                                                                                                      Q988C1
                                                                                                                                                                                                      Q8ZRZ1
                                                                                                                                                                                                                  Q92B18
                                                          16
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                                                                                                                                                                                                       16
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Matches 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                490
458
1136
457
467
622
317
470
541
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462
386
3434
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1093
537
386
400
528
531
387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue-eye;
109.5
109.5
108.5
108.5
108.5
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Q96F59
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08xmc0 clostridium
08x673 escherichia
0938q7 lactobacill
08zha9 yersinia pe
08xtx3 salmonella
08xtu5 escherichia
08xtu5 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9da75 mus musculu Q8yqv7 anabaena sp Q8r8x3 thermoanaer Q8xpl3 clostridium Q97dq0 clostridium Q97h5 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296f59 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29brc8 homo sapien
                                                                                              (without alignments)
2696.274 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                         2384
1 WMLRWALSLPPSSCLWAEPG......DEASSSGCSETDSTELASIL
                                                                               June 19, 2003, 17:45:17; Search time 35 Seconds
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                              summaries
                                                        - protein search, using sw model
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09A7H5
097L68
08XMC0
08XK73
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Q8X4U5
Q8XDK7
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Q8YQV7
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                  sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum Match 100%
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372 VPFLILVALMERNLIVITYVVAVAAGVSVAAAFLLPWSMLPDVIDDFHLKHPHSPGTEPIF 431
                                                                                                  267 SATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVA----LMESNLIITYAVAVAAGIS 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 VAAAFLLPWSMLPDVI--DDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDF
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A Kaneko T., Nakamura Y., Wolk C.P., Kawashima K., Kimura T.,
A Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
Tomplete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003594; BAB75404.1;
RIGROMS: TIGRO0792; 9ph; 1.
RIGRAMS: TIGRO0792; 9ph; 1.
W Hypothetical protein; Complete proteome.

SEQUENCE 487 AA: 54313 MW; 5C5280IDC071A47E CRC64;
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NCBI_TaxID=103690;
                                                                                                                                                                      LFKMYPIDEERRRQNKKALQALRDEASSSGCSETDSTELASIL 458
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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1D 08 YOY7
08 B DT 01
01 DT 01
01 DT 01
01 DT 01
02 B B DT 01
03 B B DT 01
04 B B DT 01
05 B B DT 01
06 B B DT 01
07 B B DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 LTAFKYVFLNKAFLPFVVGGFFAKFLLTSVPAAIPFFTKYVLRIPEKEVSLLLGSIFVTA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 AFILLPWSMLPDVIDD----FHLKQPHFHGTEPIFFSFYVFFTKFASGVSLGISTLSLDFA 381
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                                                                                                                                                                                  Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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STRAIN-MB4T, JCM11007;

MEDLINE-21992816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).

EMBL; AE013144; AAM25111.1; -.
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Bacteria; Firmloutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
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                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Na+/melibiose symporter and related transporters.
MELE OR TTE1932.
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Last annotation update)
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455 AA.
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STRAIN-13 / TYPE A;
PubMed=11792842;
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6.1%; Score 144.5; DB (0.9%; Pred. No. 0.0024;
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                                                                                                                                                                                                                                                                                                                                              STRAIN=13 / TYPE PubMed=11792842;
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Glucuronide p
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                                                                                                                                  236 FMLVEG----NFVLFCTYTLGF-RNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 IDDFHLKQPHFHGT -- EPIFFSFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVK 395
                                                                                                                                                                                                                                                                       ---GVDKTGLLYAIVTGTVKLGYALAVAVFIALGWMGFDPK-VSTPEGDAALIGM-YAIA 454
                                  -----AVILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLA
                                                                                                    229 MGWFIVILLPITVLLAVMTVKEPAAPPQHGKTGLKQYWRLLMR--PSVQRL---LFADLL
                                                                                                                                                             284 MGLAPGIAGTLFLFFFFRIKGFDKTQAGVLLLVYFLAALAGAPLWPMLAKKLGKHKALVV
                                                                                                                                                                                           GISSAVPFLIL----VALMESNLITTYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQP
                                                                                                                                                                                                             347 HFHGTEPIFFSFYVFFTKFASGVSLGIST-LSLDFAGYQTRGCSQPERVKFTLNMLVTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; Pubmed-11466286;

MeDLINE-21359325; Pubmed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qlu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

"Bacterium L183:4823-4838(2001).

EMBL: AB007584; AAK7667.1.;

InterPro: IPR001927; Na/Gal_Symp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 YLLAAGVIVCIYIICAVILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 YPVVAGIMGLIGILSFYMTYKNTREVVAPAENVKKEKITPKSIAVTIFTNRALLTLILMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 - LFTSLAFMLVEGNFVLFCTYTLGFRNEFQNLLLAIMLS-----ATLTIPIWQWFLTRFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTAVYVGISSAVPFLILVALMESNLII-----TYAVAVAAG-ISVAAAFLLPWSMLPDV
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                                                                                                                                                                                                                                                                                                               PIVLILLGLLLFKMYPIDEERRRQNKKALQALRDEA---SSSGCSETDS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 145; DB 16; Length 449;
Pred, No. 0.0022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         v1-UCT-2001 (TYEMBLrel. 18, Created)
01-OCT-2001 (TYEMBLrel. 18, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Permease of the Na+: galactoside symporter family.
CACO694.
               SSTVASQSANHTHGTTSHRETQKAY -- LLAAGVIVCIYIIC
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SEQUENCE 449 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 KSKIASAIGGSLCGYİLAYIGY----TANESQSAFTLNGIHLIQTLVPCAIVIISFILLR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SANITRSSSGKTKIVTSARTV--AYVGNFIILTSTIPLVSIIGNWQTVAIIYVCFATIFT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-LSYSSLPLMIVINFISGIFDGAGYITLTSMVADCVEYGEWKTG--KRSEGMIFSLNIF 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LAAGVIVCIYIICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 VILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCTYTLGFRNEFQ-NLLLAIMLSATLTIPIWQWFLT-RFGKKTAVYVGI--SSAVPFLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 WYTAFGIREIKDNY-AKKKEKOGFKOFINLLKTNKPLRIVLLSMLVLELSGSIKNTISIY
                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 454;
                                                                                                                                         Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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EMBL, AP003188; BAB80475.1; -
InterPro; IPR001927; Na/Gal_symp.
TIGRFAMS; TIGRO0792; ppi; 1.
Sugar transport; Complete proteome.
SEQUENCE 454 AA; 49661 MW; 9EDB58F22755A90E CRC64;
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Last sequence update)
Last annotation update)
Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
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NCBI_TaxID=83334;
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Best Local S:
Matches 69
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STRAINE-LT2 / SGS1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
MCDLINE-21534948 PubMed=11677609;
MCClelland M., Sanderson K.E., Spheth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
                                                                              MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Fersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLGTAIQGQIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLYALSDIPFW-----SMSTVMTDEPQERAKTATCAMLGVNAG-----I
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Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 477;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative permease of the Na+:galactoside symporter family
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                                                                                                                                                                                                                                                                                                                                                                                                               66643207E7686DAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%; Score 132.5; DB
18.7%; Pred. No. 0.022;
iive 78; Mismatches 1
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(TrEMBLrel. 20, Last seq
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                                                                                                                                                                                                                                                                                               Nature 413.523-527(2001).
EMBL; AJ414145; CAC89838.1; -.
InterPro; IPR001927; Na/Gal_symp.
TIGREAMS; TIGR00792; gph; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             477 AA; 53203 MW;
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Salmonella typhimurium
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Matches 73; Conserv
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 477 AA;
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01-MAR-2002 (
01-MAR-2002 (
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102 TEQTERDSATAYRMTVEVLGTVLGTAIQGQI---VGQADTPCFQDFNSSTVASQSANHTH 158
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                                                                                                                                                                                                                                                                                                                                                                ; Score 131.5; DB 16; Length 444;
; Pred. No. 0.025;
60; Mismatches 160; Indels 59;
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                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 444 AA; 49680 MW; A0E6BFD55C60700E CRC64;
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shikimate.
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                                                                                                                                                   Nature 413:852-856(2001).
EMBL; AE008890; AALZ2905.1; -.
InterPro; IPR001927; Na/Gal_symp.
TIGRPAMS; TIGR00792; gph: 1.
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